

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,356  
Source: IFWP  
Date Processed by STIC: 5/25/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/25/2006

PATENT APPLICATION: US/10/579,356

TIME: 09:32:55

Input Set : A:\D6547SEQ.txt

Output Set: N:\CRF4\05252006\J579356.raw

2 <110> APPLICANT: Gregor, Polly  
 3 Concetti, Antonio  
 4 Houghton, Alan  
 5 Venanzi, Franco Maria  
 7 <120> TITLE OF INVENTION: Compositions and Methods for Synergistic  
 8 Induction of Antitumor Immunity  
 10 <130> FILE REFERENCE: D6547  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,356  
 12 <141> CURRENT FILING DATE: 2006-05-12  
 14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/038022  
 15 <151> PRIOR FILING DATE: 2004-11-15  
 17 <160> NUMBER OF SEQ ID NOS: 13  
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 21 <211> LENGTH: 5220  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: artificial sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: nucleotide sequence for mouse TEM8  
 28 <400> SEQUENCE: 1  
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 30 tggccctatc ccggcagctc cacacagcag aacgccctgg gtccctgaaa 100  
 31 ctcgaaaccc gggctcagaa ccagcggaaa ccaaagcgaa atccttgaac 150  
 32 ttctctgaac aattgcttcc gggcgcttgc tgagagccgg gggacctgac 200  
 33 cggagccacg ccgcggtatg gcgcgcccct gatgtcacac ggacgccagc 250  
 34 gaggccagcg ctccggtcgc agcatggacc gcgcggggcg cctgggtgcg 300  
 35 ggectgcggg gactctgcgt ggctgcactc gtgctcgtgt gcgcgggaca 350  
 36 cgggggcccgc cgcgaggatg ggggaccagc ttgctacgga ggattcgacc 400  
 37 tctacttcat cctggacaag tcaggaagtg tgctgcacca ctggaatgaa 450  
 38 atctactact tcgtggagca gttggctcat agattcatca gccacagct 500  
 39 aaggatgtcc ttcatgtct tctctactcg agggacaact ttaatgaaac 550  
 40 taactgagga cagggaacag atccgacaag gcctagaaga gctccagaaa 600  
 41 gttctgccag gaggagacac ttacatgcac gaaggattcg agagggccag 650  
 42 tgagcagatt tactatgaga acagtcaagg atacaggacg gcgagcgtca 700  
 43 tcatcgcgtt gacggatggg gagctgcacg aggacctctt cttctactca 750  
 44 gagagggagg ctaaccgatc ccgagacctt ggtgcgattg ttactgcgt 800  
 45 tggcgtgaag gatttcaatg aaactcagtt ggctcggatt gcagacagta 850  
 46 aggaccacgt gtttctctgtg aacgacggct tccaggctct ccaaggcatt 900  
 47 atccactcaa ttttaaagaa atcctgcacg gaaattcttg cggctgaacc 950  
 48 atccaccatc tgccgaggag agtcctttca agtggtcgta agaggaaatg 1000  
 49 gcttccgaca tgcccgcatt gtggacaggg tctctgcag cttcaaaatc 1050  
 50 aatgactcag tcacgctcaa tgagaagccc tttgctgtgg aagacactta 1100  
 51 tttgctgtgc ccagcaccaa tcttgaaaga agttggcatg aaagctgcac 1150  
 52 tgcaggtcag catgaacgac ggctgtcct tcactccag ttctgtcatc 1200

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53 atcaccacca cacactgttc agacggctcc atcctggcga ttgctctgct 1250
54 ggtcctcttc ctgctgctgg cctggcgct gctctggtgg ttctggcccc 1300
55 tctgctgcac agtgatcatc aaggaggctc ctccaccccc tgttgaggag 1350
56 agtgaggaag aagacgatga tggtttgcca aagaagaaat ggcccacagt 1400
57 agatgcctct tattatggtg gacgcggtgt gggaggcatt aaaagaatgg 1450
58 aggtccgctg gggagaaaag ggctccacag aagaaggggc gaagttagaa 1500
59 aaggcaaaga atgcacgagt caagatgcc aagcaagaat atgagttccc 1550
60 agaaccocga aacctcaaca acaacatgcg cgggccttcc tcgcctcgga 1600
61 agtggtactc gcccatacag ggaaaactcg atgccttgtg ggttctgctg 1650
62 agaaaaggat atgaccgagt gtctgtgatg aggccacagc caggagacac 1700
63 gggacgctgt atcaacttca ccagagtga gaacagtcag ccagccaagt 1750
64 atcccctgaa caacacctac caccacagct cccacacctc cgctcctatc 1800
65 tacacacccc caccacctgc tccccactgc cctccccag cccccagtgc 1850
66 cccactcct cccattcctt cccaccatc cactctcccc cctcctctc 1900
67 agggccccacc ccctaacagg gcacctcccc cctcccgacc tctccaagg 1950
68 ccttctgtct agaaccaaa gtccgagctc tgggctgcct gagcaactcc 2000
69 agcaggaggc ttctctgctg aaagaaagat ctgcccagcc tatgtggtga 2050
70 gtggcggtct atgtttgcac gatttaaaag caagtcgtga tgggcagaa 2100
71 aaaatgggca ttttgaactg cctgaagaca gacaatgaga caataacagt 2150
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84 aaggttctc atcttcaaat acccaggacc ccagagattt ctaaatccag 2800
85 ctaagagaca gtagtcctga cttggcaaga aaaccattcc cagttgtttt 2850
86 actctgaaac aggcggtgt atgtatggta tatctctcct tggcctttca 2900
87 acctgtcac aagtattacc agttatgaag caaggagaaa tacatccagt 2950
88 gtgtaataga aaagctctgc ccacaatccc catgtcactc ctctacatta 3000
89 ttctgaagct gcttggtcag tgagcccttt aacctcatgt agactctgga 3050
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93 taaaacgggc ataagttttt atgttttggg ctgtgatctc caaagatcct 3250
94 tcaagaactc aagttagcct cattcttcca gcttgttttag aacagaggca 3300
95 tccaggtgtc atgcactcca tagacaccaa tcttgttccc caaggcagac 3350
96 attattaatc aatctcagca ctagtctcca atttaatcca attatatttt 3400
97 tccacagtac ttcacatctc ttatgacctg ttggtcatca gttagaattg 3450
98 agagagataa aactgtttg taatccctac cttagaaaga aaagcagagg 3500
99 agaattgggg aaccaccagc ataaaagtta ttatctgggg aaaatcgacc 3550
100 tgaaagaacg ccaagtcca agacctatgg tgctgacacc aaagtaacac 3600
101 tttcccaagt gtacccaga cccactctt ctccctgtgg ccaccactcc 3650

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104 aatgtctcag ccacctgaga tgacattgct gggccccaga aaaccattcc 3800
105 aaggagaatg ggctccccag gctcagagca tgcaactatg agcccatggc 3850
106 aactgttttg actgctggca gtacaaaacg ggccacccca cattacagct 3900
107 gcaggatttg tgcagccata agaaagtatg aaccaagatg ctggtgttgc 3950
108 tgttcaacaa gcatgggctt cggggaaggc agcagactcc gagagcaggc 4000
109 cttgtgcagt gtcccaaggg gctgtggtga agtgtctgag gaaaaatgaa 4050
110 tgctgataca tggtgattct gagaagaatt tgcaaggttt gaccttagaa 4100
111 tttatggaat gtcttccttg gtcattcaga attatggcta gaagtttcta 4150
112 gaaaccgtca aggttaatac ctttcagagt aggtgattac aggcaggaag 4200
113 agctttgatg tggtttacia agcccatcag ttctgtgtca ttccctgtaa 4250
114 gcaacaggag atggtggttg tgattagcaa actgcatgtg ttatttgttt 4300
115 gactccttgt tattgtcctt acggaggatt ttttttatat aagccaaatt 4350
116 ttgttgtata tattcatatt ccacgtgaca gatggaagca cgtcctatca 4400
117 gtgtgaataa aaagaacagt ttagttaaatt tattaaagcc agtgatttca 4450
118 tggcagggtta ccctaccaag ctgtgcttgt tgatctccca tgaccatact 4500
119 gctttttacia tgtacaaata gttcctaggt gacgagaccc tcctttacat 4550
120 aatgccgatg acagccttgc tgggaactgc ggtccttctg ctgtgacagc 4600
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127 caaagcctga tcttactcac caggaggatg gaaagggttt ttttagttat 4950
128 ctgagctcag ctgagttatc acgcttggag aaccgattta aaggaattag 5000
129 aatatgattt ctgaatacac ataacattaa actcttctct ttttctatgg 5050
130 taatttagtt atggacgttc agcgtctctg agttattgtt ataaaagact 5100
131 tgtcatcacc gcactgtgct gtaggagact gggctgaacc tgtacaatgg 5150
132 tataccctgg aagttgcttt tttaaaaaaa aataataata aacacctaaa 5200
133 atcaaaaaaa aaaaaaaaaa 5220
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137 <211> LENGTH: 561
138 <212> TYPE: PRT
139 <213> ORGANISM: artificial sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: amino acid sequence for mouse TEM8
144 <400> SEQUENCE: 2
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147 Val Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg
148           20              25              30
149 Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe
150           35              40              45
151 Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile
152           50              55              60
153 Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln
154           65              70              75

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157	Met	Lys	Leu	Thr	Glu	Asp	Arg	Glu	Gln	Ile	Arg	Gln	Gly	Leu	Glu
158					95					100					105
159	Glu	Leu	Gln	Lys	Val	Leu	Pro	Gly	Gly	Asp	Thr	Tyr	Met	His	Glu
160					110					115					120
161	Gly	Phe	Glu	Arg	Ala	Ser	Glu	Gln	Ile	Tyr	Tyr	Glu	Asn	Ser	Gln
162					125					130					135
163	Gly	Tyr	Arg	Thr	Ala	Ser	Val	Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu
164					140					145					150
166	Leu	His	Glu	Asp	Leu	Phe	Phe	Tyr	Ser	Glu	Arg	Glu	Ala	Asn	Arg
167					155					160					165
168	Ser	Arg	Asp	Leu	Gly	Ala	Ile	Val	Tyr	Cys	Val	Gly	Val	Lys	Asp
169					170					175					180
170	Phe	Asn	Glu	Thr	Gln	Leu	Ala	Arg	Ile	Ala	Asp	Ser	Lys	Asp	His
171					185					190					195
172	Val	Phe	Pro	Val	Asn	Asp	Gly	Phe	Gln	Ala	Leu	Gln	Gly	Ile	Ile
173					200					205					210
174	His	Ser	Ile	Leu	Lys	Lys	Ser	Cys	Ile	Glu	Ile	Leu	Ala	Ala	Glu
175					215					220					225
176	Pro	Ser	Thr	Ile	Cys	Ala	Gly	Glu	Ser	Phe	Gln	Val	Val	Val	Arg
177					230					235					240
178	Gly	Asn	Gly	Phe	Arg	His	Ala	Arg	Asn	Val	Asp	Arg	Val	Leu	Cys
179					245					250					255
180	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	Thr	Leu	Asn	Glu	Lys	Pro	Phe
181					260					265					270
182	Ala	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	Pro	Ala	Pro	Ile	Leu	Lys
183					275					280					285
184	Glu	Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser	Met	Asn	Asp	Gly
185					290					295					300
186	Leu	Ser	Phe	Ile	Ser	Ser	Ser	Val	Ile	Ile	Thr	Thr	Thr	His	Cys
187					305					310					315
188	Ser	Asp	Gly	Ser	Ile	Leu	Ala	Ile	Ala	Leu	Leu	Val	Leu	Phe	Leu
189					320					325					330
190	Leu	Leu	Ala	Leu	Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	Cys	Cys
191					335					340					345
192	Thr	Val	Ile	Ile	Lys	Glu	Val	Pro	Pro	Pro	Pro	Val	Glu	Glu	Ser
193					350					355					360
194	Glu	Glu	Glu	Asp	Asp	Asp	Gly	Leu	Pro	Lys	Lys	Lys	Trp	Pro	Thr
195					365					370					375
196	Val	Asp	Ala	Ser	Tyr	Tyr	Gly	Gly	Arg	Gly	Val	Gly	Gly	Ile	Lys
197					380					385					390
198	Arg	Met	Glu	Val	Arg	Trp	Gly	Glu	Lys	Gly	Ser	Thr	Glu	Glu	Gly
199					395					400					405
200	Ala	Lys	Leu	Glu	Lys	Ala	Lys	Asn	Ala	Arg	Val	Lys	Met	Pro	Glu
201					410					415					420
202	Gln	Glu	Tyr	Glu	Phe	Pro	Glu	Pro	Arg	Asn	Leu	Asn	Asn	Asn	Met
203					425					430					435
204	Arg	Arg	Pro	Ser	Ser	Pro	Arg	Lys	Trp	Tyr	Ser	Pro	Ile	Lys	Gly

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205          440          445          450
206 Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp Arg
207          455          460          465
208 Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Arg Cys Ile Asn
209          470          475          480
210 Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
211          485          490          495
212 Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr
213          500          505          510
214 Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala
215          515          520          525
216 Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro
217          530          535          540
218 Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro
219          545          550          555
220 Pro Pro Arg Pro Ser Val
221          560
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 252
226 <212> TYPE: PRT
227 <213> ORGANISM: artificial sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: amino acids 27-279 for mouse TEM8
232 <400> SEQUENCE: 3
233 Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp
234          5          10          15
235 Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp
236          20          25          30
237 Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe Ile
238          35          40          45
239 Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly
240          50          55          60
241 Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln
242          65          70          75
243 Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr
244          80          85          90
245 Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu
246          95          100          105
247 Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr
248          110          115          120
250 Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu
251          125          130          135
252 Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly
253          140          145          150
254 Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
255          155          160          165
256 Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln
257          170          175          180
258 Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu

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VERIFICATION SUMMARY

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DATE: 05/25/2006

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L:12 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION NUMBER: is Added.